



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 25, 2026 – 12:23 AM EDT

PDB ID : 1OFA / pdb\_00001ofa  
Title : Crystal structure of the tyrosine-regulated 3-deoxy-d-arabino-heptulosonate-7-phosphate synthase from *saccharomyces cerevisiae* in complex with phosphoenolpyruvate and cobalt(ii)  
Authors : Koenig, V.; Pfeil, A.; Heinrich, G.; Braus, G.H.; Schneider, T.R.  
Deposited on : 2003-04-09  
Resolution : 2.02 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

---

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

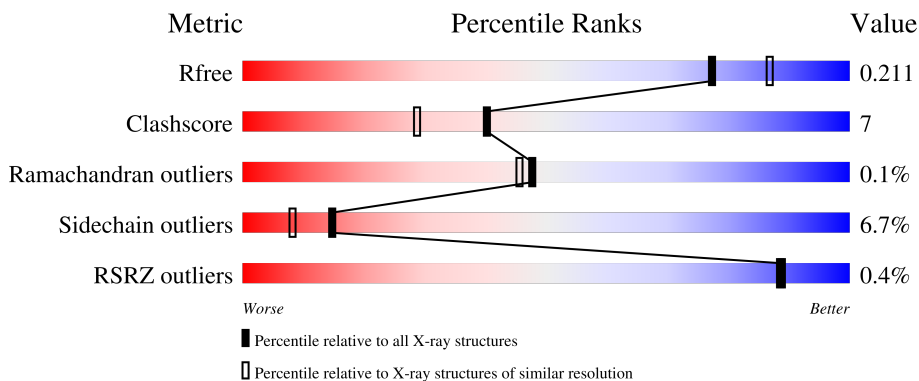
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.02 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	180053	13299 (2.04-2.00)
Clashscore	190562	1022 (2.02-2.02)
Ramachandran outliers	187476	1014 (2.02-2.02)
Sidechain outliers	187428	1014 (2.02-2.02)
RSRZ outliers	180081	13314 (2.04-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	370	 72% 16% 7%
1	B	370	 70% 18% 9%

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 5481 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

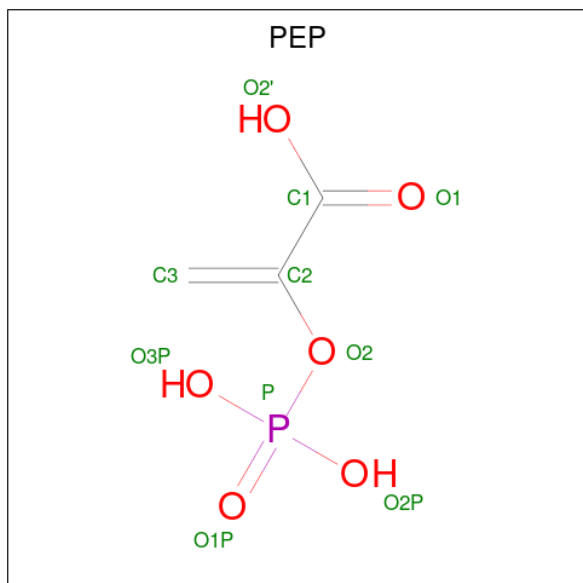
- Molecule 1 is a protein called PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	343	Total 2592	C 1615	N 467	O 500	S 10	0	0	0
1	B	338	Total 2560	C 1593	N 462	O 495	S 10	0	0	0

- Molecule 2 is COBALT (II) ION (CCD ID: CO) (formula: Co).

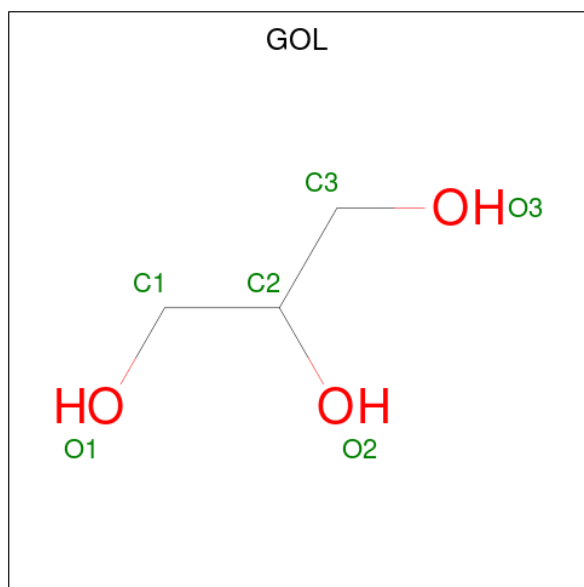
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 1	Co 1	0	0
2	B	1	Total 1	Co 1	0	0

- Molecule 3 is PHOSPHOENOLPYRUVATE (CCD ID: PEP) (formula: C<sub>3</sub>H<sub>5</sub>O<sub>6</sub>P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	0	0
			10	3	6	1		
3	B	1	Total	C	O	P	0	0
			10	3	6	1		

- Molecule 4 is GLYCEROL (CCD ID: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		

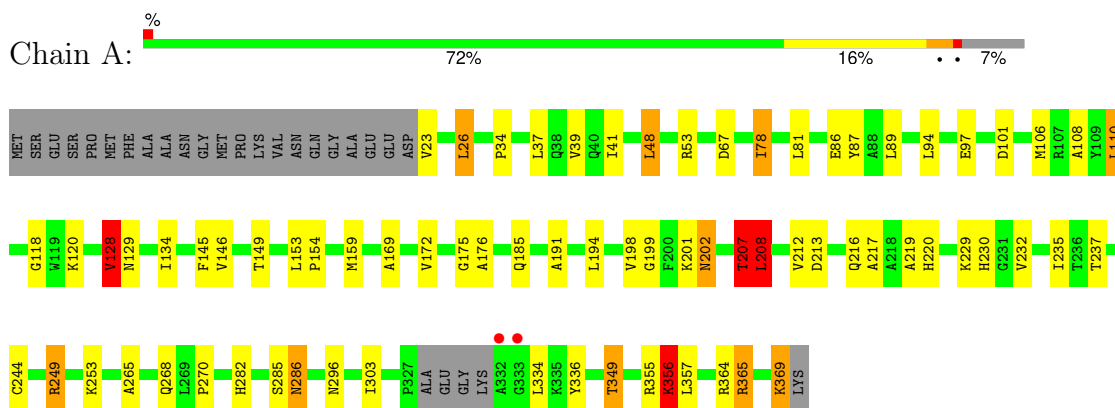
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	145	Total	O	0	0
			145	145		
5	B	144	Total	O	0	0
			144	144		

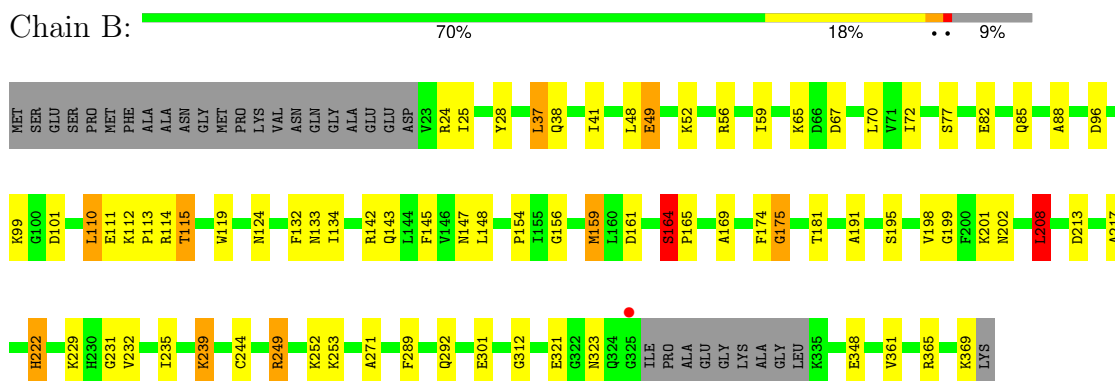
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE



- Molecule 1: PHOSPHO-2-DEHYDRO-3-DEOXYHEPTONATE ALDOLASE



## 4 Data and refinement statistics i

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	196.21Å 50.61Å 64.98Å 90.00° 106.33° 90.00°	Depositor
Resolution (Å)	17.57 – 2.02 17.57 – 2.02	Depositor EDS
% Data completeness (in resolution range)	97.1 (17.57-2.02) 97.1 (17.57-2.02)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.54 (at 2.02Å)	Xtrriage
Refinement program	REFMAC 5.1.19	Depositor
R, $R_{free}$	0.155 , 0.204 0.162 , 0.211	Depositor DCC
$R_{free}$ test set	1971 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	26.3	Xtrriage
Anisotropy	0.090	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 40.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.016 for -h-2*1,-k,l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5481	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	26.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.43% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, PEP, CO

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z  > 5$	RMSZ	# $ Z  > 5$
1	A	1.61	23/2630 (0.9%)	1.38	12/3560 (0.3%)
1	B	1.63	23/2597 (0.9%)	1.43	17/3514 (0.5%)
All	All	1.62	46/5227 (0.9%)	1.40	29/7074 (0.4%)

The worst 5 of 46 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	169	ALA	CA-CB	10.48	1.71	1.53
1	B	159	MET	SD-CE	-9.97	1.54	1.79
1	A	146	VAL	CA-CB	9.58	1.66	1.54
1	A	303	ILE	CA-CB	7.78	1.63	1.54
1	A	159	MET	SD-CE	-7.73	1.60	1.79

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	208	LEU	CB-CG-CD2	-7.84	87.17	110.70
1	B	99	LYS	N-CA-C	6.04	119.75	112.38
1	B	124	ASN	N-CA-C	5.79	117.59	111.28
1	A	175	GLY	O-C-N	-5.76	118.07	123.48
1	A	149	THR	OG1-CB-CG2	-5.72	97.86	109.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2592	0	2612	43	0
1	B	2560	0	2575	42	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	10	0	2	0	0
3	B	10	0	2	0	0
4	A	6	0	8	0	0
4	B	12	0	16	1	0
5	A	145	0	0	0	1
5	B	144	0	0	1	1
All	All	5481	0	5215	69	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

The worst 5 of 69 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:208:LEU:CD1	1:A:208:LEU:CG	1.76	1.59
1:A:356:LYS:NZ	1:A:356:LYS:CE	1.68	1.52
1:A:232:VAL:HG12	1:B:232:VAL:HG12	1.19	1.15
1:A:97:GLU:OE1	1:A:355:ARG:NH1	1.95	0.98
1:A:78:ILE:HD11	1:A:108:ALA:HA	1.41	0.98

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:2108:HOH:O	5:B:2047:HOH:O[1_565]	2.03	0.17

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	339/370 (92%)	328 (97%)	11 (3%)	0	100	100
1	B	334/370 (90%)	323 (97%)	10 (3%)	1 (0%)	36	31
All	All	673/740 (91%)	651 (97%)	21 (3%)	1 (0%)	48	45

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	195	SER

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	278/298 (93%)	254 (91%)	24 (9%)	10	4
1	B	275/298 (92%)	262 (95%)	13 (5%)	23	16
All	All	553/596 (93%)	516 (93%)	37 (7%)	15	8

5 of 37 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	115	THR
1	B	253	LYS
1	B	164	SER
1	B	208	LEU
1	A	208	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	38	GLN
1	B	323	ASN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	85	GLN
1	B	324	GLN
1	B	296	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 2 are monoatomic - leaving 5 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	PEP	A	508	-	9,9,9	2.80	4 (44%)	11,13,13	1.56	3 (27%)
4	GOL	A	601	-	5,5,5	0.64	0	5,5,5	0.88	0
4	GOL	B	601	-	5,5,5	0.59	0	5,5,5	1.04	1 (20%)
3	PEP	B	508	-	9,9,9	2.80	4 (44%)	11,13,13	1.56	3 (27%)
4	GOL	B	603	-	5,5,5	0.84	0	5,5,5	1.82	2 (40%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PEP	A	508	-	-	0/9/9/9	-
4	GOL	A	601	-	-	0/4/4/4	-
4	GOL	B	601	-	-	2/4/4/4	-
3	PEP	B	508	-	-	0/9/9/9	-
4	GOL	B	603	-	-	2/4/4/4	-

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	508	PEP	P-O2	-5.28	1.50	1.59
3	B	508	PEP	P-O2	-5.28	1.50	1.59
3	B	508	PEP	C2-C1	3.47	1.52	1.49
3	A	508	PEP	C2-C1	3.45	1.52	1.49
3	B	508	PEP	P-O1P	-3.16	1.40	1.50

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	603	GOL	O2-C2-C3	2.88	121.12	109.18
3	A	508	PEP	O3P-P-O2	-2.77	97.24	105.32
3	B	508	PEP	O3P-P-O2	-2.77	97.26	105.32
4	B	603	GOL	C3-C2-C1	-2.37	103.10	111.80
3	A	508	PEP	O2P-P-O2	2.31	112.06	105.32

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	603	GOL	C1-C2-C3-O3
4	B	603	GOL	O2-C2-C3-O3
4	B	601	GOL	C1-C2-C3-O3
4	B	601	GOL	O2-C2-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	603	GOL	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled '#RSRZ > 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q < 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	343/370 (92%)	-0.67	2 (0%) 85 86	18, 25, 38, 52	0
1	B	338/370 (91%)	-0.72	1 (0%) 90 90	17, 24, 36, 48	0
All	All	681/740 (92%)	-0.69	3 (0%) 88 89	17, 25, 37, 52	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	332	ALA	3.8
1	B	325	GLY	2.5
1	A	333	GLY	2.1

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	GOL	B	603	6/6	0.90	0.09	36,42,44,44	0
4	GOL	A	601	6/6	0.93	0.07	28,30,36,36	0

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	PEP	B	508	10/10	0.96	0.07	21,24,30,32	0
4	GOL	B	601	6/6	0.97	0.05	23,28,29,29	0
3	PEP	A	508	10/10	0.98	0.05	21,24,30,32	0
2	CO	B	400	1/1	1.00	0.04	27,27,27,27	0
2	CO	A	400	1/1	1.00	0.02	26,26,26,26	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.